

130-5
FILE COPY
**RAW SEQUENCE LISTING
ERROR REPORT**

OFFICE OF
SYSTEMS
BRANCH

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5

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/601,168

Source: Batch

Date Processed by STIC: 10-5-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE - SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BATCH

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/601,168

DATE: 10/05/2000
 TIME: 14:54:23

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\10052000\I601168.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: BENAROUS, Richard
 4 MARGOTTIN, Florence
 5 DURAND, Herve
 6 ARENZANA SEISDEDOS, Fernando
 7 KROLL, Mathias
 8 CONDORCET, Jean-Paul
 10 <120> TITLE OF INVENTION: Human (TrCP protein for targeting proteins towards
 11 proteasome degradation pathways
 W--> 0 <130> FILE REFERENCE:
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/601,168
 C--> 14 <141> CURRENT FILING DATE: 2000-07-28
 16 <150> PRIOR APPLICATION NUMBER: FR98 01100
 17 <151> PRIOR FILING DATE: 1998-01-30
 19 <150> PRIOR APPLICATION NUMBER: FR98 15545
 20 <151> PRIOR FILING DATE: 1998-12-09
 22 <160> NUMBER OF SEQ ID NOS: 8
 24 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 2151
 E--> 28 <212> TYPE: ADN
 29 <213> ORGANISM: Artificial sequence
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (70)..(1776)
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: Description of the artificial sequence : ADNc
 37 coding for human (TrCP protein
 39 <400> SEQUENCE: 1
 40 tgcgtggct gggctggc accaaagggg cggcccccggc ggagagcggg cccagtggcc 60
 42 tcggcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag 111
 43 Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys
 44 1 5 10
 46 ttt atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct 159
 47 Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro
 48 15 20 25 30
 50 agg aag ata ata cca gag aag aat tca ctt aga cag aca tac aac agc 207
 51 Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser
 52 35 40 45
 54 tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act 255
 55 Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr
 56 50 55 60
 58 gct atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc 303
 59 Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly

Global error:

Valid responses for <212> type
 are DNA, RNA, or PRT

→ CDNA?

RAW SEQUENCE LISTING

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\10052000\I601168.raw

60	65	70	75						
62	act tcc	agt atg	att gtg	ccc aag caa cgg	aaa ctc tca	gca agc	tat	351	
63	Thr Ser	Ser Met	Ile Val	Pro Lys	Gln Arg	Lys Leu	Ser Ala	Ser Tyr	
64	80		85		90				
66	gaa aag	gaa aag	gaa ctg	tgt gtc	aaa tac	ttt gag	cag tgg	tca gag	399
67	Glu Lys	Glu Lys	Glu Leu	Cys Val	Lys Tyr	Phe Glu	Gln Trp	Ser Glu	
68	95		100		105		110		
71	tca gat	caa gtg	gaa ttt	gtg gaa	cat ctt	ata tcc	caa atg	tgt cat	447
72	Ser Asp	Gln Val	Glu Phe	Val Glu	His Leu	Ile Ser	Gln Met	Cys His	
73		115		120		125			
75	tac caa	cat ggg	cac ata	aac tcg	tat ott	aaa cct	atg ttg	cag aga	495
76	Tyr Gln	His Gly	His Ile	Asn Ser	Tyr Leu	Lys Pro	Met Leu	Gln Arg	
77		130		135		140			
79	gat ttc	ata act	gct ctg	cca gct	cgg gga	ttt gat	cat atc	gct gag	543
80	Asp Phe	Ile Thr	Ala Leu	Pro Ala	Arg Gly	Leu Asp	His Ile	Ala Glu	
81		145		150		155			
83	aac att	ctg tca	tac ctg	gtt gac	aaa tca	cta tgt	gtt gct	gaa ctt	591
84	Asn Ile	Leu Ser	Tyr Leu	Asp Ala	Lys Ser	Leu Cys	Ala Ala	Glu Leu	
85		160		165		170			
87	gtg tgc	aag gaa	tgg tac	cga gtg	acc tct	gat ggc	atg ctg	tgg aag	639
88	Val Cys	Lys Glu	Trp Tyr	Arg Val	Thr Ser	Asp Gly	Met Leu	Trp Lys	
89	175		180		185		190		
91	aag ctt	atc gag	aga atg	gtc agg	aca gat	tct ctg	tgg aga	ggc ctg	687
92	Lys Leu	Ile Glu	Arg Met	Val Arg	Thr Asp	Ser Leu	Trp Arg	Gly Leu	
93		195		200		205			
95	gca gaa	cga aga	gga tgg	gga cag	tat ttc	aaa aac	aaa cct	cct	735
96	Ala Glu	Arg Arg	Gly Trp	Gly Gln	Tyr Leu	Phe Lys	Asn Lys	Pro Pro	
97		210		215		220			
99	gac ggg	aat gct	cct ccc	aac tct	ttt tat	aga gca	ctt tat	cct aaa	783
100	Asp Gly	Asn Ala	Pro Pro	Asn Ser	Phe Tyr	Arg Ala	Leu Tyr	Pro Lys	
101		225		230		235			
103	att ata	caa gac	att gag	aca ata	gaa tct	aat tgg	aga tgt	gga aga	831
104	Ile Ile	Gln Asp	Ile Glu	Thr Ile	Glu Ser	Asn Trp	Arg Cys	Gly Arg	
105		240		245		250			
107	cat agt	tta cag	aga att	cac tgc	cga agt	gaa aca	agc aaa	gga gtt	879
108	His Ser	Leu Gln	Arg Ile	His Cys	Arg Ser	Glu Thr	Ser Lys	Gly Val	
109	255		260		265		270		
111	tac tgt	tta cag	tat gat	gtt cag	aaa ata	gta agc	ggc ctt	cga gac	927
112	Tyr Cys	Leu Gln	Tyr Asp	Asp Gln	Lys Ile	Val Ser	Gly Leu	Arg Asp	
113		275		280		285			
115	aac aca	atac atc	tgg gat	aaa aac	aca ttg	gaa tgc	aat cgt	aaa att	975
116	Asn Thr	Ile Lys	Ile Trp	Asp Lys	Asn Thr	Leu Glu	Cys Lys	Arg Ile	
117		290		295		300			
119	ctc aca	ggc cat	aca ggt	tca gtc	ctc tgt	ctc cag	tat gat	gat gag	1023
120	Leu Thr	Gly His	Thr Gly	Ser Val	Leu Cys	Leu Gln	Tyr Asp	Glu Arg	
121		305		310		315			
123	gtg atc	ata aca	gga tca	tcg gat	tcc acg	gtc aga	gtg tgg	gat gta	1071
124	Val Ile	Ile Thr	Gly Ser	Ser Asp	Ser Thr	Val Arg	Val Trp	Asp Val	
125		320		325		330			

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Input Set : A:\PTO.txt
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127 aat aca ggt gaa atg cta aac acg ttg att cac cat tgt gaa gca gtt	1119
128 Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val	
129 335 340 345 350	350
132 ctg cac ttg cgt ttc aat aat ggc atg atg gtc acc tgc tcc aaa gat	1167
133 Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp	
134 355 360 365	365
136 cgt tcc att gct gta tgg gat atg gcc tcc cca act gac att acc ctc	1215
137 Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu	
138 370 375 380	380
140 cgg agg gtc gtc gga cac cga gct gtc aat gtt gta gac ttt	1263
141 Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe	
142 385 390 395	395
144 gat gac aag tac att gtt tct gca tct ggg gat aga act ata aag gta	1311
145 Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val	
146 400 405 410	410
148 tgg aac aca agt act tgt gaa ttt gta agg acc tta aat gga cac aaa	1359
149 Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys	
150 415 420 425 430	430
152 cga ggc att gcc tgt ttg cag tac agg gac agg ctg gta gtc agt ggc	1407
153 Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly	
154 435 440 445	445
156 tca tct gac aac act atc aga tta tgg gac ata gaa tgt ggt gca tgt	1455
157 Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys	
158 450 455 460	460
160 tta cga gtg tta gaa ggc cat gag gaa ttt gtc cgt tgt att cga ttt	1503
161 Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe	
162 465 470 475	475
164 gat aac aag agg ata gtc agt ggg gcc tat gat gga aaa att aaa gtc	1551
165 Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val	
166 480 485 490	490
168 tgg gat ctt gtg gct gtc ttg gac ccc cgt gct cct gca ggg aca ctc	1599
169 Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu	
170 495 500 505 510	510
172 tgt cta cgg acc ctt gtg gag cat tcc gga aga gtt ttt cga cta cag	1647
173 Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln	
174 515 520 525	525
176 ttt gat gaa ttc cag att gtc agt agt tca cat gat gac aca atc ctc	1695
177 Phe Asp Glu Phe Gln Ile Val Ser Ser His Asp Asp Thr Ile Leu	
178 530 535 540	540
180 atc tgg gac ttc cta aat gat cca gct gcc caa gct gaa ccc ccc cgt	1743
181 Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg	
182 545 550 555	555
184 tcc cct tct cga aca tac acc tac atc tcc aga taaataacca tacactgacc	1796
185 Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg	
186 560 565	565
188 tcatacttgc ccaggaccca ttaaagggtgc ggtatcttac gttatctgcca ataccaggat	1856
190 gagcaacaac agtaacaatc aactactgc ccagtttccc tggactagcc gaggagcagg	1916
192 gctttqagac tccgttggg acacagttgg tctgcgtcg gcccaggacg gtctactcag	1976
194 cacaactgac tgcttcagtg ctgcatacg aagatgtctt ctatcaattg tgaatgattt	2036

RAW SEQUENCE LISTING
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Input Set : A:\PTO.txt
 Output Set: N:\CRF3\10052000\I601168.raw

196 gaactttaa acctcccttc ctctccctt ttcacccctg cacctagtt tttccattg 2096
 198 gttccagaca aagggtgactt ataaatataat ttagtgtttt gccagaaaa aaaaa. 2151
 322 <210> SEQ ID NO: 3
 323 <211> LENGTH: 19
 E--> 324 <212> TYPE: ADN
 325 <213> ORGANISM: Artificial sequence
 327 <220> FEATURE:
 328 <223> OTHER INFORMATION: Description of the artificial sequence : sense primer
 330 <400> SEQUENCE: 3
 331 cccaaactgcg tataaacgcg 19
 334 <210> SEQ ID NO: 4
 335 <211> LENGTH: 20
 E--> 336 <212> TYPE: ADN
 337 <213> ORGANISM: Artificial sequence
 339 <220> FEATURE:
 340 <223> OTHER INFORMATION: Description of the artificial sequence : antisense primer
 342 <400> SEQUENCE: 4
 343 ggtgaatcaa cgtgttttagc 20
 346 <210> SEQ ID NO: 5
 347 <211> LENGTH: 20
 E--> 348 <212> TYPE: ADN
 349 <213> ORGANISM: Artificial sequence
 351 <220> FEATURE:
 352 <223> OTHER INFORMATION: Description of the artificial sequence : sense primer
 354 <400> SEQUENCE: 5
 355 ggatgatgtataaactatc 20
 358 <210> SEQ ID NO: 6
 359 <211> LENGTH: 25
 E--> 360 <212> TYPE: ADN
 361 <213> ORGANISM: Artificial sequence
 363 <220> FEATURE:
 364 <223> OTHER INFORMATION: Description of the artificial sequence : antisense primer
 366 <400> SEQUENCE: 6
 367 ttatcccaag atcttgattt tgttg 25
 370 <210> SEQ ID NO: 7
 371 <211> LENGTH: 30
 E--> 372 <212> TYPE: ADN
 373 <213> ORGANISM: Artificial sequence
 375 <220> FEATURE:
 376 <223> OTHER INFORMATION: Description of the artificial sequence : primer
 378 <400> SEQUENCE: 7
 379 ccaggatcttataacaatc tgacagcagc 30
 382 <210> SEQ ID NO: 8
 383 <211> LENGTH: 29
 E--> 384 <212> TYPE: ADN
 385 <213> ORGANISM: Artificial sequence
 387 <220> FEATURE:
 388 <223> OTHER INFORMATION: Description of the artificial sequence : primer
 390 <400> SEQUENCE: 8

Refer
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 P.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/601,168

DATE: 10/05/2000

TIME: 14:54:23

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10052000\I601168.raw

391 ccaggatcct tagtcccaga tgaggattg
398 1

29

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/601,168

DATE: 10/05/2000
TIME: 14:54:24

Input Set : A:\PTO.txt
Output Set: N:\CRF3\10052000\I601168.raw

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:324 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:336 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:348 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:360 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:372 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:384 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: